

Das erat- SEQ ID 10-1

RESULT 4

US-10-275-998-10

; Sequence 10, Application US/10275998

; Publication No. US20040023354A1

; GENERAL INFORMATION:

; APPLICANT: INCYTE GENOMICS, INC.

; APPLICANT: DAS, Debopriya

; APPLICANT: REDDY, Roopa

; APPLICANT: YAO, Monique G.

; APPLICANT: NGUYEN, Danniell B.

; APPLICANT: LU, Yan

; APPLICANT: TRIBOULEY, Catherine M.

; APPLICANT: YUE, Henry

; APPLICANT: KHAN, Farrah A.

; APPLICANT: GANDHI, Ameena R.

; APPLICANT: AU-YOUNG, Janice

; APPLICANT: LAL, Preeti

; APPLICANT: KEARNEY, Liam

; APPLICANT: ELLIOTT, Vicki S.

; APPLICANT: DING, Li

; APPLICANT: THORNTON, Michael

; TITLE OF INVENTION: LIPID METABOLISM ENZYMES

; FILE REFERENCE: PI-0095 USN

; CURRENT APPLICATION NUMBER: US/10/275,998

; CURRENT FILING DATE: 2002-11-08

; PRIOR APPLICATION NUMBER: US 01/15210

; PRIOR FILING DATE: 2001-05-11

; PRIOR APPLICATION NUMBER: US 60/203,511

; PRIOR FILING DATE: 2000-05-11

; PRIOR APPLICATION NUMBER: US 60/207,903

; PRIOR FILING DATE: 2000-05-25

; PRIOR APPLICATION NUMBER: US 60/210,150

; PRIOR FILING DATE: 2000-06-07

; PRIOR APPLICATION NUMBER: US 60/213,392

; PRIOR FILING DATE: 2000-06-23

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: PERL Program

; SEQ ID NO 10

; LENGTH: 4237

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; OTHER INFORMATION: Incyte ID No. US20040023354A1 7472768CB1

US-10-275-998-10

Query Match 79.5%; Score 3684.6; DB 8; Length 4237;

Best Local Similarity 94.6%; Pred. No. 0;

Matches 3926; Conservative 0; Mismatches 4; Indels 219; Gaps 2;

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Qy      546 GTGGAGCGGTGCATGGGTGCCATGCAAGAGGGGATGCAGATGGTGAAGCTGCGTGGCGGC 605
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Db      87  GTGGAGCGGTGCATGGGTGCCATGCAAGAGGGGATGCAGATGGTGAAGCTGCGTGGCGGC 146

Qy      606 TCCAAGGGCCTGGTCCGCTTCTACTACCTGGACGAGCACCGCTCCTGCATCCGCTGGAGG 665
          |||
Db      147 TCCAAGGGCCTGGTCCGCTTCTACTACCTGGACGAGCACCGCTCCTGCATCCGCTGGAGG 206

Qy      666 CCCTCACGCAAGAACGAGAAGGCCAAGATCTCCATCGACTCCATCCAGGAGGTGAGTGAG 725
          |||
Db      207 CCCTCACGCAAGAACGAGAAGGCCAAGATCTCCATCGACTCCATCCAGGAGGTGAGTGAG 266

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Qy	726	GGGCGGCAGTCGGAGGTCTTCAGCGCTACCTGACGGCAGCTTCGACCCCAACTGCTGC	785
Db	267	GGGCGGCAGTCGGAGGTCTTCAGCGCTACCTGACGGCAGCTTCGACCCCAACTGCTGC	326
Qy	786	TTCAGCATCTACCACGGCAGCCACCGCGAGTCGCTGGACCTGGTCTCCACCAGCAGCGAG	845
Db	327	TTCAGCATCTACCACGGCAGCCACCGCGAGTCGCTGGACCTGGTCTCCACCAGCAGCGAG	386
Qy	846	GTGGCGCGCACCTGGGTCACTGGCTGCGCTACCTCATGGCCGGCATCAGCGACGAGGAC	905
Db	387	GTGGCGCGCACCTGGGTCACTGGCTGCGCTACCTCATGGCCGGCATCAGCGACGAGGAC	446
Qy	906	AGCCTGGCTCGCCGCCAGCGCACCAGGGACC-----	936
Db	447	AGCCTGGCTCGCCGCCAGCGCACCAGGGACCAATATCCTTGGGCACCTATCGGGCAATGC	506
Qy	937	-----	936
Db	507	AGACCCAGGGACCGGCCCTTGGCTGCTCACCTGGGGGGCCTGTCTTTGCCGGGTCA	566
Qy	937	-----AGTGGCTGAAGCAGACGTTTGACGAGGCC	965
Db	567	CACACTGGGGAAGTGGCCGGCCAGAGGGTGGAGTGGCTGAAGCAGACGTTTGACGAGGCC	626
Qy	966	GACAAGAACGGGGATGGCAGCCTGAGCATTTGGCGAGGTCTGCAGCTGCTGCACAAGCTC	1025
Db	627	GACAAGAACGGGGATGGCAGCCTGAGCATTTGGCGAGGTCTGCAGCTGCTGCACAAGCTC	686
Qy	1026	AACGTGAACCTGCCCCGGCAGAGGGTGAAGCAGATGTTTCAG-----	1066
Db	687	AACGTGAACCTGCCCCGGCAGAGGGTGAAGCAGATGTTTCAGGGTGGCTGGTCATGCCTGG	746
Qy	1067	-----	1066
Db	747	CTGGAGCAAGGGAAGCTGGCCTGCTCACAGGACAGGGCCCTGGTTCGAGGTGCCAATGGGG	806
Qy	1067	-----GGAAGCGGACACGGATGACCACCAAGGGACGCTGGGTTTT	1106
Db	807	ACCCAAGGCCTTGCAATTGCAGGAAGCGGACACGGATGACCACCAAGGGACGCTGGGTTTT	866
Qy	1107	GAAGAGTTCTGTGCCTTCTACAAGATGATGTCCACCCGCCGGGACCTCTACCTGCTCATG	1166
Db	867	GAAGAGTTCTGTGCCTTCTACAAGATGATGTCCACCCGCCGGGACCTCTACCTGCTCATG	926
Qy	1167	CTGACCTACAGCAACCACAAGGACACCTGGATGCCGCCAGCCTGCAGCGCTTCCTGCAG	1226
Db	927	CTGACCTACAGCAACCACAAGGACACCTGGATGCCGCCAGCCTGCAGCGCTTCCTGCAG	986
Qy	1227	GTGGAGCAGAAGATGGCGGGTGTGACCTCGAGAGCTGCCAGGACATCATCGAGCAGTTT	1286
Db	987	GTGGAGCAGAAGATGGCGGGTGTGACCTCGAGAGCTGCCAGGACATCATCGAGCAGTTT	1046
Qy	1287	GAGCCATGCCCAGAAAAAAGAGTAAGGGGCTGCTGGGCATTGATGGCTTACCAACTAC	1346
Db	1047	GAGCCATGCCCAGAAAAAAGAGTAAGGGGCTGCTGGGCATTGATGGCTTACCAACTAC	1106
Qy	1347	ACCAGGAGCCCTGCTGGTGACATCTTCAACCCTGAGCACCACCATGTGCACCAGGACATG	1406
Db	1107	ACCAGGAGCCCTGCTGGTGACATCTTCAACCCTGAGCACCACCATGTGCACCAGGACATG	1166

Qy	14 07	ACGCAGCCGCTGAGCCACTACTTCATCACCTCGTCCCAACACCTACCTCGTGGGTGAC	14 66
Db	11 67	ACGCAGCCGCTGAGCCACTACTTCATCACCTCGTCCCAACACCTACCTCGTGGGTGAC	12 26
Qy	14 67	CAGCTCATGTCCCAGTCACGGGTGGACATGTATGCTTGGGTCCTGCAGGCTGGCTGCCGC	15 26
Db	12 27	CAGCTCATGTCCCAGTCACGGGTGGACATGTATGCTTGGGTCCTGCAGGCTGGCTGCCGC	12 86
Qy	15 27	TGCGTGGAGGTGGACTGCTGGGATGGGCCCGACGGGGAGCCCATTGTGCACCATGGCTAC	15 86
Db	12 87	TGCGTGGAGGTGGACTGCTGGGATGGGCCCGACGGGGAGCCCATTGTGCACCATGGCTAC	13 46
Qy	15 87	ACTCTGACTTCCAAGATCCTCTTCAAAGACGTATTGAAACCATCAACAAATATGCCTTC	16 46
Db	13 47	ACTCTGACTTCCAAGATCCTCTTCAAAGACGTATTGAAACCATCAACAAATATGCCTTC	14 06
Qy	16 47	ATCAAGAATGAGTACCCAGTGATCCTGTCCATCGAAAACCACTGCAGTGTATCCAGCAG	17 06
Db	14 07	ATCAAGAATGAGTACCCAGTGATCCTGTCCATCGAAAACCACTGCAGTGTATCCAGCAG	14 66
Qy	17 07	AAGAAAATGGCCCAGTATCTGACTGACATCCTTGGGGACAAGCTGGACCTGTATCAGTG	17 66
Db	14 67	AAGAAAATGGCCCAGTATCTGACTGACATCCTTGGGGACAAGCTGGACCTGTATCAGTG	15 26
Qy	17 67	AGCAGTGAAGATGCCACCACACTCCCTCTCCACAGATGCTCAAGGGCAAGATCCTCGTG	18 26
Db	15 27	AGCAGTGAAGATGCCACCACACTCCCTCTCCACAGATGCTCAAGGGCAAGATCCTCGTG	15 86
Qy	18 27	AAGGGGAAGAAGCTCCCAGCCAACATCAGCGAGGATGCGGAGGAAGGCGAGGTGTCTGAT	18 86
Db	15 87	AAGGGGAAGAAGCTCCCAGCCAACATCAGCGAGGATGCGGAGGAAGGCGAGGTGTCTGAT	16 46
Qy	18 87	GAGGACAGTGCTGATGAGATTGACGATGACTGCAAGCTCCTCAATGGGGATGCATCCACC	19 46
Db	16 47	GAGGACAGTGCTGATGAGATTGACGATGACTGCAAGCTCCTCAATGGGGATGCATCCACC	17 06
Qy	19 47	AATCGAAAGCGTGTAAGAAAACACTGCTAAGAGGAACTGGATTCCCTCATCAAAGAGTCG	20 06
Db	17 07	AATCGAAAGCGTGTAAGAAAACACTGCTAAGAGGAACTGGATTCCCTCATCAAAGAGTCG	17 66
Qy	20 07	AAGATTCGGGACTGTGAGGACCCCAACAACCTTCTCCGTCTCCACACTGTCCCATCTGGA	20 66
Db	17 67	AAGATTCGGGACTGTGAGGACCCCAACAACCTTCTCCGTCTCCACACTGTCCCATCTGGA	18 26
Qy	20 67	AAGCTCGGACGCAAGAGCAAGGCTGAAGAGGACGTGGAGTCTGGGGAGGATGCCGGGGCC	21 26
Db	18 27	AAGCTCGGACGCAAGAGCAAGGCTGAAGAGGACGTGGAGTCTGGGGAGGATGCCGGGGCC	18 86
Qy	21 27	AGCAGACGCAATGGCCGCCTCGTCGTGGGAAGCTTCTCCAGGCGCAAGAAGAAGGGCAGC	21 86
Db	18 87	AGCAGACGCAATGGCCGCCTCGTCGTGGGAAGCTTCTCCAGGCGCAAGAAGAAGGGCAGC	19 46
Qy	21 87	AAGCTGAAGAAGGCGGCCAGCGTGAGGAGGGAGATGAGGGTCAGGACTCCCCGGGAGGC	22 46
Db	19 47	AAGCTGAAGAAGGCGGCCAGCGTGAGGAGGGAGATGAGGGTCAGGACTCCCCGGGAGGC	20 06
Qy	22 47	CAGAGCCGAGGGGCGACCCGGCAGAAGAAGACCATGAAGCTGTCCCGGGCCCTCTCTGAC	23 06
Db	20 07	CAGAGCCGAGGGGCGACCCGGCAGAAGAAGACCATGAAGCTGTCCCGGGCCCTCTCTGAC	20 66
Qy	23 07	CTGGTGAAGTACACCAAGTCCGTGGCCACCCACGACATAGAGATGGAGGCGGCGTCCAGC	23 66

Db	2067	CTGGTGAAGTACACCAAGTCCGTGGCCACCCACGACATAGAGATGGAGGCGGCGTCCAGC	2126
Qy	2367	TGGCAGGTGTCGTCTTCAGCGAGACCAAGGCCACAGATTCTGCAGCAGAAGCCGGCG	2426
Db	2127	TGGCAGGTGTCGTCTTCAGCGAGACCAAGGCCACAGATTCTGCAGCAGAAGCCGGCG	2186
Qy	2427	CAGTACCTACGCTTCAACCAGCAGCAGCTCTCCGCATCTACCCCTCCTCCTACCGTGTG	2486
Db	2187	CAGTACCTACGCTTCAACCAGCAGCAGCTCTCCGCATCTACCCCTCCTCCTACCGTGTG	2246
Qy	2487	GACTCCAGCAACTACAACCCGAGCCCTTCTGGAACGCCGGCTGCCAAATGGTTGCCCTG	2546
Db	2247	GACTCCAGCAACTACAACCCGAGCCCTTCTGGAACGCCGGCTGCCAAATGGTTGCCCTG	2306
Qy	2547	AACTACCAGTCAGAGGGGCGGATGCTGCAGCTGAACCGAGCCAAGTTCAGCGCCAACGGT	2606
Db	2307	AACTACCAGTCAGAGGGGCGGATGCTGCAGCTGAACCGAGCCAAGTTCAGCGCCAACGGT	2366
Qy	2607	GGCTGCGGCTACGTACTCAAGCCTGGGTGCATGTGCCAGGGCGTGTTC AACCCCAACTCG	2666
Db	2367	GGCTGCGGCTACGTACTCAAGCCTGGGTGCATGTGCCAGGGCGTGTTC AACCCCAACTCG	2426
Qy	2667	GAGGACCCCTGCCCGGGCAGCTCAAGAAGCAGCTGGTGCTCCGGATCATCAGTGGCCAG	2726
Db	2427	GAGGACCCCTGCCCGGGCAGCTCAAGAAGCAGCTGGTGCTCCGGATCATCAGTGGCCAG	2486
Qy	2727	CAGCTTCCCAAGCCGCGCGACTCCATGCTGGGGGACCGTGGGGAGATCATCGACCCCTT	2786
Db	2487	CAGCTTCCCAAGCCGCGCGACTCCATGCTGGGGGACCGTGGGGAGATCATCGACCCCTT	2546
Qy	2787	GTGGAGGTGGAGATCATTGGGCTCCCTGTGGACTGCAGCAGGGAGCAGACCCGCGTGGTG	2846
Db	2547	GTGGAGGTGGAGATCATTGGGCTCCCTGTGGACTGCAGCAGGGAGCAGACCCGCGTGGTG	2606
Qy	2847	GACGACAACGGGTTCAACCCACCTGGGAGGAGACCCTGGTTTTCATGGTGCACATGCCG	2906
Db	2607	GACGACAACGGGTTCAACCCACCTGGGAGGAGACCCTGGTTTTCATGGTGCACATGCCG	2666
Qy	2907	GAGATCGCGCTGGTCCGCTTCTCGTCTGGGACCACGATCCCATCGGGCGTGACTTCATT	2966
Db	2667	GAGATCGCGCTGGTCCGCTTCTCGTCTGGGACCACGATCCCATCGGGCGTGACTTCATT	2726
Qy	2967	GGCCAGAGGACGCTGGCCTTTCAGCAGCATGATGCCAGGCTACAGACACGTGTACCTAGAA	3026
Db	2727	GGCCAGAGGACGCTGGCCTTTCAGCAGCATGATGCCAGGCTACAGACACGTGTACCTGGAG	2786
Qy	3027	GGGATGGAAGAGGCCTCCATCTTCGTGCATGTGGCTGTCAGTGACATCAGCGGTAAGGTC	3086
Db	2787	GGGATGGAAGAGGCCTCCATCTTCGTGCATGTGGCTGTCAGTGACATCAGCGGTAAGGTC	2846
Qy	3087	AAGCAGGCTCTGGGCCTAAAAGGCCTCTTCCTCCGAGGCCAAAGCCCGGCTCGCTGGAC	3146
Db	2847	AAGCAGGCTCTGGGCCTAAAAGGCCTCTTCCTCCGAGGCCAAAGCCCGGCTCGCTGGAC	2906
Qy	3147	AGTCATGCTGCTGGGCGGCCCCCGGCCCGGCCCTCCGTTAGCCAGCGGATCCTGCGGCGC	3206
Db	2907	AGTCATGCTGCTGGGCGGCCCCCGGCCCGGCCCTCCGTTAGCCAGCGGATCCTGCGGCGC	2966
Qy	3207	ACGGCCAGCGCCCCGACCAAGAGCAGAAGCCGGGCCGAGGGGCTTCCCGGAGCTGGTC	3266

Db	2967	ACGGCCAGCGCCCCGACCAAGAGCCAGAAGCCGGGCCGCGAGGGGCTTCCCGGAGCTGGTC	3026
Qy	3267	CTGGGTACACGGGACACAGGCTCCAAGGGGTGGCAGACGATGTGGTGCCCCCGGGCCC	3326
Db	3027	CTGGGTACACGGGACACAGGCTCCAAGGGGTGGCAGACGATGTGGTGCCCCCGGGCCC	3086
Qy	3327	GGACCTGCTCCGGAAGCCCCAGCCCAGGAGGGGCCCGGCAGCGGCAGCCCCGAGGTAAG	3386
Db	3087	GGACCTGCTCCGGAAGCCCCAGCCCAGGAGGGGCCCGGCAGCGGCAGCCCCGAGGTAAG	3146
Qy	3387	GCGCCAGCTGCGGTGGCAGAGAAGAGCCCTGTGCGAGTGCGGCCCCCGCGTGCTCTGGAC	3446
Db	3147	GCGCCAGCTGCGGTGGCAGAGAAGAGCCCTGTGCGAGTGCGGCCCCCGCGTGCTCTGGAC	3206
Qy	3447	GGCCCCGGGCCTGCTGGGATGGCCGCCACATGCATGAAGTGTGTGGTGGGATCCTGCGCC	3506
Db	3207	GGCCCCGGGCCTGCTGGGATGGCCGCCACATGCATGAAGTGTGTGGTGGGATCCTGCGCC	3266
Qy	3507	GGCGTGAACACCGGGGGCCTGCAGAGGGAGCGGCCACCCAGCCCCGGGGCCTGCAAGCAGG	3566
Db	3267	GGCGTGAACACCGGGGGCCTGCAGAGGGAGCGGCCACCCAGCCCCGGGGCCTGCAAGCAGG	3326
Qy	3567	CAGGCAGCCATTCGCCAGCAGCCCCGGGGCCGGGCTGACTCACTGGGGGCCCCCTGCTGT	3626
Db	3327	CAGGCAGCCATTCGCCAGCAGCCCCGGGGCCGGGCTGACTCACTGGGGGCCCCCTGCTGT	3386
Qy	3627	GGCCTGGACCTCACGCTATCCCGGGGAGAAGCAGAGAGGCCCCCAAGGGTCCTGGGGCC	3686
Db	3387	GGCCTGGACCTCACGCTATCCCGGGGAGAAGCAGAGAGGCCCCCAAGGGTCCTGGGGCC	3446
Qy	3687	TGGAGGCAGGGTCCAGGCGGTAGCGGCTCCATGTCTCGGACTCCAGCAGCCAGACAGC	3746
Db	3447	TGGAGGCAGGGTCCAGGCGGTAGCGGCTCCATGTCTCGGACTCCAGCAGCCAGACAGC	3506
Qy	3747	CCGGGCATCCCCGAAAGGTCCCCCGCTGGCCTGAGGGTGCTTCAGGCAACCGGGGGCC	3806
Db	3507	CCGGGCATCCCCGAAAGGTCCCCCGCTGGCCTGAGGGTGCTTCAGGCAACCGGGGGCC	3566
Qy	3807	CTGCAGGGAGAGATGAGTGCTTGTGCTCAAAAGCTGGAGGAGATCAGGAGTAAATCC	3866
Db	3567	CTGCAGGGAGAGATGAGTGCTTGTGCTCAAAAGCTGGAGGAGATCAGGAGTAAATCC	3626
Qy	3867	CCCATGTTCTTCGCCGGTAAGCCCCTCTGCCCTGCGTGGTTCCTCCCGCAGCCCCCTGGC	3926
Db	3627	CCCATGTTCTTCGCCGGTAAGCCCCTCTGCCCTGCGTGGTTCCTCCCGCAGCCCCCTGGC	3686
Qy	3927	ATGGCTGGGCCTGGGTACCTGCTGCTGCTTCTGCGTGGACGGTGTGCGCTCGTGTGCTC	3986
Db	3687	ATGGCTGGGCCTGGGTACCTGCTGCTGCTTCTGCGTGGACGGTGTGCGCTCGTGTGCTC	3746
Qy	3987	GTGCTCGTGGCTCTGTATCCGTGGCACTGTCTCCGTGGCACTCTGCTCCCTTGGCTTGCC	4046
Db	3747	GTGCTCGTGGCTCTGTATCCGTGGCACTGTCTCCGTGGCACTCTGCTCCCTTGGCTTGCC	3806
Qy	4047	TGTGGCCCATAGCCCCAGCCCTCCTGTCTGAGCTTGAGGCCCTGGGACTTGGGTGGAGCT	4106
Db	3807	TGTGGCCCATAGCCCCAGCCCTCCTGTCTGAGCTTGAGGCCCTGGGACTTGGGTGGAGCT	3866
Qy	4107	GGTTTGAGGCCCGACAGGCTGGGAAGAACCAGCTGCTCTTGCTGAGGGTCTGGGGCCGGG	4166
Db	3867	GGTTTGAGGCCCGACAGGCTGGGAAGAACCAGCTGCTCTTGCTGAGGGTCTGGGGCCGGG	3926

Qy	4167	ACTGTGGCCTGACATGCTGGGCCCCTCCGGCTGGGCGCTTCCCCAAACTCACCTCCTGGG	4226
Db	3927	ACTGTGGCCTGACATGCTGGGCCCCTCCGGCTGGGCGCTTCCCCAAACTCACCTCCTGGG	3986
Qy	4227	CGGCTGGCGACCTGCATGGCCCCTGATGCCTTTCCTGGGACTGGGGGCCATGTACCATCC	4286
Db	3987	CGGCTGGCGACCTGCATGGCCCCTGATGCCTTTCCTGGGACTGGGGGCCACGTACCATCC	4046
Qy	4287	CATTCCCACCTCCCTCTAGGGCAGGCTCCAGGGGTCCTACTGGGAAGTCTGATGTGGGC	4346
Db	4047	CATTCCCACCTCCCTCTAGGGCAGGCTCCAGGGGTCCTACTGGGAAGTCTGATGTGGGC	4106
Qy	4347	AGGTAGTGCAGCTGCTGGGCGTCTCCTGCGCCCCCTGGGACGCCTGGAGCCTGCTGAGTGC	4406
Db	4107	AGGTAGTGCAGCTGCTGGGCGTCTCCTGCGCCCCCTGGGACGCCTGGAGCCTGCTGAGTGC	4166
Qy	4407	TGCGTGGAGTAGATTCCCTGGGCCCCAGGGCTTCGCTGCTTTGGGCTGAAGCACCCACT	4466
Db	4167	TGCGTGGAGTAGATTCCCTGGGCCCCAGGGCTTCGCTGCTTTGGGCTGAAGCACCCACT	4226
Qy	4467	AGAAGGGTG	4475
Db	4227	AGAAGGGTG	4235

Day et al - Seq ID No. 2

RESULT 4

US-10-275-998-5

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; Sequence 5, Application US/10275998
; Publication No. US20040023354A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: DAS, Debopriya
; APPLICANT: REDDY, Roopa
; APPLICANT: YAO, Monique G.
; APPLICANT: NGUYEN, Danniell B.
; APPLICANT: LU, Yan
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: YUE, Henry
; APPLICANT: KHAN, Farrah A.
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: LAL, Preeti
; APPLICANT: KEARNEY, Liam
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: DING, Li
; APPLICANT: THORNTON, Michael
; TITLE OF INVENTION: LIPID METABOLISM ENZYMES
; FILE REFERENCE: PI-0095 USN
; CURRENT APPLICATION NUMBER: US/10/275,998
; CURRENT FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: US 01/15210
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/203,511
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/207,903
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/210,150
; PRIOR FILING DATE: 2000-06-07
; PRIOR APPLICATION NUMBER: US 60/213,392
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PERL Program
; SEQ ID NO 5
; LENGTH: 1239
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20040023354A1 7472768CD1
US-10-275-998-5
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Query Match          95.5%; Score 6092.5; DB 4; Length 1239;
Best Local Similarity 94.1%; Pred. No. 0;
Matches 1166; Conservative 0; Mismatches 0; Indels 73; Gaps 2;
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Qy      42 MGAMQEGMQMVKLRGGSKGLVRFYYLDEHRSCIRWRPSRKNEKAKISIDSIQEVSEGRQS 101
      |||
Db       1 MGAMQEGMQMVKLRGGSKGLVRFYYLDEHRSCIRWRPSRKNEKAKISIDSIQEVSEGRQS 60

Qy     102 EVFQRYPDGSFDPNCCFSIYHGSHRESLDLVSTSSEVARTWVTGLRYLMAGISDEDSLAR 161
      |||
Db      61 EVFQRYPDGSFDPNCCFSIYHGSHRESLDLVSTSSEVARTWVTGLRYLMAGISDEDSLAR 120

Qy     162 RQRTRDQ-----WLKQTFDEADKNG 181
      |||
Db     121 RQRTRDQYPWAPIGQCRPRDRPLGCSPWGGLSFAGSHTGEVAGQRVWLKQTFDEADKNG 180
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Qy	182	DGSLSIGEV LQLLHKLNVNLPQRVKQMFR-----	211
Db	181	DGSLSIGEV LQLLHKLNVNLPQRVKQMFRVAGHAWLEQGKLACSQDRALVEVPMGTQGL	240
Qy	212	---EADTDDHQGT LGFE EFCAFYKMMSTRDLYLLMLTYSNHKDHLDAASLQRF LQVEQK	268
Db	241	ALQEADTDDHQGT LGFE EFCAFYKMMSTRDLYLLMLTYSNHKDHLDAASLQRF LQVEQK	300
Qy	269	MAGVTLESCQDI IEQFEPCPENKSKGLLGIDGFTNYTRSPAGDI FNPEHHHVHQDMTQPL	328
Db	301	MAGVTLESCQDI IEQFEPCPENKSKGLLGIDGFTNYTRSPAGDI FNPEHHHVHQDMTQPL	360
Qy	329	SHYFITSSHNTYLVGDQLMSQSRVDMYAWVLQAGCRCVEVDCWDGPDGEP IVHHGYTLTS	388
Db	361	SHYFITSSHNTYLVGDQLMSQSRVDMYAWVLQAGCRCVEVDCWDGPDGEP IVHHGYTLTS	420
Qy	389	KILFKDVIETINKYAFI KNEYPVI LSIENHCSVIQQKKMAQYLTDI LGDKLDLSSVSSD	448
Db	421	KILFKDVIETINKYAFI KNEYPVI LSIENHCSVIQQKKMAQYLTDI LGDKLDLSSVSSD	480
Qy	449	ATTLPSPQMLKGKILVKGKKLPANISED AEEGEVSDEDSADEIDDDCKLLNGDASTNRKR	508
Db	481	ATTLPSPQMLKGKILVKGKKLPANISED AEEGEVSDEDSADEIDDDCKLLNGDASTNRKR	540
Qy	509	VENTAKRKLDSL I KESKIRDCEDPNNFSVSTLSPSGKLGRKSKAEEDVESGEDAGASRRN	568
Db	541	VENTAKRKLDSL I KESKIRDCEDPNNFSVSTLSPSGKLGRKSKAEEDVESGEDAGASRRN	600
Qy	569	GRLVVGFSFRRKKKGSKL KKAASVEEGDEGQDSPGGQSRGATRQKKTMKLSRALSDLVKY	628
Db	601	GRLVVGFSFRRKKKGSKL KKAASVEEGDEGQDSPGGQSRGATRQKKTMKLSRALSDLVKY	660
Qy	629	TKSVATHDIEMEAASSWQVSSFSETKAHQI LQQKPAQYLRFNQQQLSRIYPSSYRVDSSN	688
Db	661	TKSVATHDIEMEAASSWQVSSFSETKAHQI LQQKPAQYLRFNQQQLSRIYPSSYRVDSSN	720
Qy	689	YNPQPFWNAGCQMVALNYQSEGRMLQLNRAKFSANGGCGYVLKPGCMCQGVFNPNSEDPL	748
Db	721	YNPQPFWNAGCQMVALNYQSEGRMLQLNRAKFSANGGCGYVLKPGCMCQGVFNPNSEDPL	780
Qy	749	PGQLKKQLVLR I ISGQQLPKPRDSMLGDRGEI IDPFVEVEI IGLPVDCSREQTRVDDNG	808
Db	781	PGQLKKQLVLR I ISGQQLPKPRDSMLGDRGEI IDPFVEVEI IGLPVDCSREQTRVDDNG	840
Qy	809	FNPTWEETLVFMVHMPEIALVRFLVWDHDP IGRDFI GQRTLAFSSMMPGYRHVYLEGMEE	868
Db	841	FNPTWEETLVFMVHMPEIALVRFLVWDHDP IGRDFI GQRTLAFSSMMPGYRHVYLEGMEE	900
Qy	869	ASIFVHVAVSDISGKVKQALGLKGLFLRGPKPGSLD SHAAGRPPARPSVSQRILRRTASA	928
Db	901	ASIFVHVAVSDISGKVKQALGLKGLFLRGPKPGSLD SHAAGRPPARPSVSQRILRRTASA	960
Qy	929	PTKSQKPGRRGFPELV LGTRDTGSKGVADDVVP GP GPAPAEAPAE GPGSGSPRGKAPAA	988
Db	961	PTKSQKPGRRGFPELV LGTRDTGSKGVADDVVP GP GPAPAEAPAE GPGSGSPRGKAPAA	1020
Qy	989	VAEKSPVRVRP PRVL DGPAGMAATCMKCVVGS CAGVNTGGLQRRERPPSPGPASRQAAI	1048
Db	1021	VAEKSPVRVRP PRVL DGPAGMAATCMKCVVGS CAGVNTGGLQRRERPPSPGPASRQAAI	1080

Qy	1049	RQQPRARADSLGAPCCGLDPHAIPGRSREAPKGP	QAWRQGP	GGSGSMSSDSSSPDSPGIP	1108
Db	1081	RQQPRARADSLGAPCCGLDPHAIPGRSREAPKGP	QAWRQGP	GGSGSMSSDSSSPDSPGIP	1140
Qy	1109	ERSPRWPEGACRQPGALQGEMSALFAQLEEIRSKSPMFSAGKPLLPCVVLP	HAPGMAGP	1168	
Db	1141	ERSPRWPEGACRQPGALQGEMSALFAQLEEIRSKSPMFSAGKPLLPCVVLP	HAPGMAGP	1200	
Qy	1169	GSPAAASAWTVSPRVLVLVALYPWHCLRG	TLLPWLACGP	1207	
Db	1201	GSPAAASAWTVSPRVLVLVALYPWHCLRG	TLLPWLACGP	1239	

Qy	973	ACGCAGCCGCTGAGCCACTACTTCATCACCTCGTCCCAACACCTACCTCGTGGGTGAC	1032
Db	1167	ACGCAGCCGCTGAGCCACTACTTCATCACCTCGTCCCAACACCTACCTCGTGGGTGAC	1226
Qy	1033	CAGCTCATGTCCCAGTCACGGGTGGACATGTATGCTTGGGTCCTGCAGGCTGGCTGCCGC	1092
Db	1227	CAGCTCATGTCCCAGTCACGGGTGGACATGTATGCTTGGGTCCTGCAGGCTGGCTGCCGC	1286
Qy	1093	TGCGTGGAGGTGGACTGCTGGGATGGGCCGACGGGGAGCCATTGTGCACCATGGCTAC	1152
Db	1287	TGCGTGGAGGTGGACTGCTGGGATGGGCCGACGGGGAGCCATTGTGCACCATGGCTAC	1346
Qy	1153	ACTCTGACTTCCAAGATCCTCTTCAAAGACGTCATTGAAACCATCAACAAATATGCCTTC	1212
Db	1347	ACTCTGACTTCCAAGATCCTCTTCAAAGACGTCATTGAAACCATCAACAAATATGCCTTC	1406
Qy	1213	ATCAAGAATGAGTACCCAGTGATCCTGTCCATCGAAAACCACTGCAGTGTATCCAGCAG	1272
Db	1407	ATCAAGAATGAGTACCCAGTGATCCTGTCCATCGAAAACCACTGCAGTGTATCCAGCAG	1466
Qy	1273	AAGAAAAATGGCCAGTATCTGACTGACATCCTTGGGGACAAGCTGGACCTGTATCAGTG	1332
Db	1467	AAGAAAAATGGCCAGTATCTGACTGACATCCTTGGGGACAAGCTGGACCTGTATCAGTG	1526
Qy	1333	AGCAGTGAAGATGCCACCACACTCCCTCTCCACAGATGCTCAAGGGCAAGATCCTCGTG	1392
Db	1527	AGCAGTGAAGATGCCACCACACTCCCTCTCCACAGATGCTCAAGGGCAAGATCCTCGTG	1586
Qy	1393	AAGGGGAAGAAGCTCCCAGCCAACATCAGCGAGGATGCGGAGGAAGGCGAGGTGTCTGAT	1452
Db	1587	AAGGGGAAGAAGCTCCCAGCCAACATCAGCGAGGATGCGGAGGAAGGCGAGGTGTCTGAT	1646
Qy	1453	GAGGACAGTGCTGATGAGATTGACGATGACTGCAAGCTCCTCAATGGGGATGCATCCACC	1512
Db	1647	GAGGACAGTGCTGATGAGATTGACGATGACTGCAAGCTCCTCAATGGGGATGCATCCACC	1706
Qy	1513	AATCGAAAGCGTGTAGAAAACACTGCTAAGAGGAACTGGATTCCCTCATCAAAGAGTCG	1572
Db	1707	AATCGAAAGCGTGTAGAAAACACTGCTAAGAGGAACTGGATTCCCTCATCAAAGAGTCG	1766
Qy	1573	AAGATTCGGGACTGTGAGGACCCCAACAATTCTCCGTCTCCACACTGTCCCATCTGGA	1632
Db	1767	AAGATTCGGGACTGTGAGGACCCCAACAATTCTCCGTCTCCACACTGTCCCATCTGGA	1826
Qy	1633	AAGCTCGGACGCAAGAGCAAGGCTGAAGAGGACGTGGAGTCTGGGGAGGATGCCGGGGCC	1692
Db	1827	AAGCTCGGACGCAAGAGCAAGGCTGAAGAGGACGTGGAGTCTGGGGAGGATGCCGGGGCC	1886
Qy	1693	AGCAGACGCAATGGCCGCCTCGTCGTGGGAAGCTTCTCAGGCGCAAGAAGAAGGGCAGC	1752
Db	1887	AGCAGACGCAATGGCCGCCTCGTCGTGGGAAGCTTCTCAGGCGCAAGAAGAAGGGCAGC	1946
Qy	1753	AAGCTGAAGAAGGCGGCCAGCGTGGAGGAGGGAGATGAGGGTCAGGACTCCCGGGAGGC	1812
Db	1947	AAGCTGAAGAAGGCGGCCAGCGTGGAGGAGGGAGATGAGGGTCAGGACTCCCGGGAGGC	2006
Qy	1813	CAGAGCCGAGGGGCGACCCGGCAGAAGAAGACCATGAAGCTGTCCCGGGCCCTCTCTGAC	1872
Db	2007	CAGAGCCGAGGGGCGACCCGGCAGAAGAAGACCATGAAGCTGTCCCGGGCCCTCTCTGAC	2066
Qy	1873	CTGGTGAAGTACACCAAGTCCGTGGCCACCCACGACATAGAGATGGAGGCGGCGTCCAGC	1932

Db	2067	CTGGTGAAGTACACCAAGTCCGTGGCCACCCACGACATAGAGATGGAGGCGGCGTCCAGC	2126
Qy	1933	TGGCAGGTGTCGTCCCTTCAGCGAGACCAAGGCCACAGATTCTGCAGCAGAAGCCGGCG	1992
Db	2127	TGGCAGGTGTCGTCCCTTCAGCGAGACCAAGGCCACAGATTCTGCAGCAGAAGCCGGCG	2186
Qy	1993	CAGTACCTACGCTTCAACCAGCAGCAGCTCTCCCGCATCTACCCCTCCTCCTACCGTGTG	2052
Db	2187	CAGTACCTACGCTTCAACCAGCAGCAGCTCTCCCGCATCTACCCCTCCTCCTACCGTGTG	2246
Qy	2053	GACTCCAGCAACTACAACCCGAGCCCTTCTGGAACGCCGGCTGCCAAATGGTTGCCCTG	2112
Db	2247	GACTCCAGCAACTACAACCCGAGCCCTTCTGGAACGCCGGCTGCCAAATGGTTGCCCTG	2306
Qy	2113	AACTACCAGTCAGAGGGGCGGATGCTGCAGCTGAACCGAGCCAAGTTCAGCGCCAACGGT	2172
Db	2307	AACTACCAGTCAGAGGGGCGGATGCTGCAGCTGAACCGAGCCAAGTTCAGCGCCAACGGT	2366
Qy	2173	GGCTGCGGCTACGTACTCAAGCCTGGGTGCATGTGCCAGGGCGTGTTCACCCCAACTCG	2232
Db	2367	GGCTGCGGCTACGTACTCAAGCCTGGGTGCATGTGCCAGGGCGTGTTCACCCCAACTCG	2426
Qy	2233	GAGGACCCCTGCCCGGGCAGCTCAAGAAGCAGCTGGTGCTCCGGATCATCAGTGGCCAG	2292
Db	2427	GAGGACCCCTGCCCGGGCAGCTCAAGAAGCAGCTGGTGCTCCGGATCATCAGTGGCCAG	2486
Qy	2293	CAGCTTCCCAAGCCGCGCGACTCCATGCTGGGGGACCGTGGGGAGATCATCGACCCCTTT	2352
Db	2487	CAGCTTCCCAAGCCGCGCGACTCCATGCTGGGGGACCGTGGGGAGATCATCGACCCCTTT	2546
Qy	2353	GTGGAGGTGAGATCATTGGGCTCCTGTGGACTGCAGCAGGGAGCAGACCCGCGTGGTG	2412
Db	2547	GTGGAGGTGAGATCATTGGGCTCCTGTGGACTGCAGCAGGGAGCAGACCCGCGTGGTG	2606
Qy	2413	GACGACAACGGGTTCAACCCACCTGGGAGGAGACCCTGGTTTTCATGGTGCACATGCCG	2472
Db	2607	GACGACAACGGGTTCAACCCACCTGGGAGGAGACCCTGGTTTTCATGGTGCACATGCCG	2666
Qy	2473	GAGATCGCGCTGGTCCGCTTCCTCGTCTGGGACCACGATCCCATCGGGCGTGACTTCATT	2532
Db	2667	GAGATCGCGCTGGTCCGCTTCCTCGTCTGGGACCACGATCCCATCGGGCGTGACTTCATT	2726
Qy	2533	GGCCAGAGGACGCTGGCCTTCAGCAGCATGATGCCAGGCTACAGACACGTGTACCTAGAA	2592
Db	2727	GGCCAGAGGACGCTGGCCTTCAGCAGCATGATGCCAGGCTACAGACACGTGTACCTGGAG	2786
Qy	2593	GGGATGGAAGAGGCCTTCATCTTCGTGCATGTGGCTGTCAGTGACATCAGCGGTAAGGTC	2652
Db	2787	GGGATGGAAGAGGCCTTCATCTTCGTGCATGTGGCTGTCAGTGACATCAGCGGTAAGGTC	2846
Qy	2653	AAGCAGGCTCTGGGCCTAAAAGGCCTCTTCCTCCGAGGCCCAAAGCCCGGCTCGCTGGAC	2712
Db	2847	AAGCAGGCTCTGGGCCTAAAAGGCCTCTTCCTCCGAGGCCCAAAGCCCGGCTCGCTGGAC	2906
Qy	2713	AGTCATGCTGCTGGGCGGCCCCCGGCCCGGCCCTCCGTTAGCCAGCGGATCCTGCGGCGC	2772
Db	2907	AGTCATGCTGCTGGGCGGCCCCCGGCCCGGCCCTCCGTTAGCCAGCGGATCCTGCGGCGC	2966
Qy	2773	ACGGCCAGCGCCCGACCAAGAGCCAGAAGCCGGGCCGAGGGGCTCCCGGAGCTGGTC	2832

Db	2967	ACGGCCAGCGCCCCGACCAAGAGCCAGAAGCCGGGCCGCGAGGGGCTTCCCGAGCTGGTC	3026
Qy	2833	CTGGGTACACGGGACACAGGCTCCAAGGGGTGGCAGACGATGTGGTGCCCCCGGGGCC	2892
Db	3027	CTGGGTACACGGGACACAGGCTCCAAGGGGTGGCAGACGATGTGGTGCCCCCGGGGCC	3086
Qy	2893	GGACCTGCTCCGGAAGCCCCAGCCAGGAGGGGCCCGGCAGCGGCAGCCCCGAGGTAAG	2952
Db	3087	GGACCTGCTCCGGAAGCCCCAGCCAGGAGGGGCCCGGCAGCGGCAGCCCCGAGGTAAG	3146
Qy	2953	GCGCCAGCTGCGGTGGCAGAGAAGAGCCCTGTGCGAGTGCGGCCCCCGCGTGTCTGGAC	3012
Db	3147	GCGCCAGCTGCGGTGGCAGAGAAGAGCCCTGTGCGAGTGCGGCCCCCGCGTGTCTGGAC	3206
Qy	3013	GGCCCCGGGCCTGCTGGGATGGCCGCCACATGCATGAAGTGTGTGGTGGGATCCTGCGCC	3072
Db	3207	GGCCCCGGGCCTGCTGGGATGGCCGCCACATGCATGAAGTGTGTGGTGGGATCCTGCGCC	3266
Qy	3073	GGCGTGAACACCGGGGGCCTGCAGAGGGAGCGGCCACCCAGCCCGGGGCTGCAAGCAGG	3132
Db	3267	GGCGTGAACACCGGGGGCCTGCAGAGGGAGCGGCCACCCAGCCCGGGGCTGCAAGCAGG	3326
Qy	3133	CAGGCAGCCATTCCGCAGCAGCCCCGGGCCCGGGCTGACTCACTGGGGGCCCCCTGCTGT	3192
Db	3327	CAGGCAGCCATTCCGCAGCAGCCCCGGGCCCGGGCTGACTCACTGGGGGCCCCCTGCTGT	3386
Qy	3193	GGCCTGGACCTCAGCTATCCCGGGGAGAAGCAGAGAGGCCCCCAAGGGTCCTGGGGCC	3252
Db	3387	GGCCTGGACCTCAGCTATCCCGGGGAGAAGCAGAGAGGCCCCCAAGGGTCCTGGGGCC	3446
Qy	3253	TGGAGGCAGGGTCCAGGCGGTAGCGGCTCCATGTCTCGGACTCCAGCAGCCAGACAGC	3312
Db	3447	TGGAGGCAGGGTCCAGGCGGTAGCGGCTCCATGTCTCGGACTCCAGCAGCCAGACAGC	3506
Qy	3313	CCGGGCATCCCCGAAAGGTCCCCCGCTGGCCTGAGGGTGCCTGCAGGCAACCGGGGGCC	3372
Db	3507	CCGGGCATCCCCGAAAGGTCCCCCGCTGGCCTGAGGGTGCCTGCAGGCAACCGGGGGCC	3566
Qy	3373	CTGCAGGGAGAGATGAGTGCTTGTCTGCTCAAAAGCTGGAGGAGATCAGGAGTAAATCC	3432
Db	3567	CTGCAGGGAGAGATGAGTGCTTGTCTGCTCAAAAGCTGGAGGAGATCAGGAGTAAATCC	3626
Qy	3433	CCCATGTTCTCCGCCGGTAAGCCCCTCTGCCCTGCGTGGTCCTCCCGCACGCCCTGGC	3492
Db	3627	CCCATGTTCTCCGCCGGTAAGCCCCTCTGCCCTGCGTGGTCCTCCCGCACGCCCTGGC	3686
Qy	3493	ATGGCTGGGCTGGGTACCTGCTGCTGCTCTGCGTGGACGGTGTGCGCTCGTGTGCTC	3552
Db	3687	ATGGCTGGGCTGGGTACCTGCTGCTGCTCTGCGTGGACGGTGTGCGCTCGTGTGCTC	3746
Qy	3553	GTGCTCGTGGCTCTGTATCCGTGGCACTGTCTCCGTGGCACTCTGCTCCCTTGGCTTGCC	3612
Db	3747	GTGCTCGTGGCTCTGTATCCGTGGCACTGTCTCCGTGGCACTCTGCTCCCTTGGCTTGCC	3806
Qy	3613	TGTGGCCCATAG	3624
Db	3807	TGTGGCCCATAG	3818